**JESSICA JONES**
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## SUMMARY

8+ years of experience in neuroscience and data science, skilled in machine learning models and visualization tools to extract insights from complex biological data. Deep understanding of experimental design and Python-based analytics to support data-driven discovery in biotech and precision medicine. Integrating agentic workflows to expedite productivity, advance portfolios, and enhance research.

## SKILLS

**Wetlab:** Perfusion and Fixing Dissection, IHC/in situ RNA-scope protocol, scRNAseq transcriptomics, FACs sorting and analysis, Animal Handling, Genotyping, Phenotypic Characterization

**Backend:** NumPy, pandas, FastAPI, httpx, biopython, SQLite/Alchemy, pydantic, logging, batch processing, git

**Frontend:** React 18+, Typescript, D3.js, Vite, seaborn, matplotlib, TanStack, tailwind/post CSS, networkx, plotly, altair, webGL

**Hardware:** NI-DAQ, Arduino, Raspberry Pi, Simulink

**Management:** Laboratory Safety Coordination, Project Management, Cross-Functional Team Leadership, Research Mentorship, Cross-Lab Communication

**Machine Learning:** TensorFlow, PyTorch, Scikit-learn, OpenCV**,** keras, DeepLabCut, sLEAP

## EDUCATION

**Ph.D. Neurobiology and Biophysics**, University of Washington, *Sept. 2025*
***Relevant Courses****: Computational Methods for Data Analysis (AMATH 582), Quantitative Methods in Neuroscience (NEURO 582), Data Visualization (CSE 512)*

**B.S. Molecular, Cell, Developmental (MCD) Biology,** University of California Santa Cruz, June 2018
**Awards:** *(2025) SMDP Biotech Scholar, (2022) HHMI Gilliam Fellowship, (2022) NSF-GRFP Honorable Mention, (2020) NIH T32 Predoctoral Training Program in the Neurosciences, (2017) NIH IMSD Scholar Award*

## RELEVANT WORK EXPERIENCE

**Senior Scientific Software Engineer, Visualization**, Genentech, Dec 2025 – Present
- Architected full-stack data visualization platforms combining FastAPI backend with React frontend, implementing real-time genomic association queries with support for multiple search modalities and batch processing of large-scale datasets
- Built a full-stack clinicogenomic real-world data portal using React, TypeScript, FastAPI, MongoDB, and ClickHouse, enabling researchers to define oncology cohorts, compare clinical/genomic features, and visualize survival, biomarker, treatment, and demographic outcomes.
- Designed dynamic ontology mapping system enabling automatic categorization of 4000+ phenotypes
- Optimized data query performance through batch processing architecture (200-variant chunks, 10k-annotation segments) and implemented efficient filtering/pagination logic, reducing memory footprint and enabling smooth visualization of large association datasets
- Built interactive visualization layer using D3.js SVG rendering with hybrid WebGL architecture exploration, enabling filtering and plot implementation with hover tooltips

**Research Associate**, University of Washington, Aug 2020 – Dec 2025
- Analyzed large-scale connectome and single-cell RNA-seq data
- Implemented machine learning models for neuronal circuit tracing
- Engineered computer vision algorithms for behavioral tracking
- Taught and mentored students in neurobiology and biophysics, and presented at major conferences

**Research Assistant,** University of Pennsylvania, Aug 2018 – Aug 2020
- Led the development of an automated motor reflex tracking system using ML/computer vision,
- Built a statistical modeling package for pain-state assessment, reducing manual analysis time by 98%;
- Mentored REU students and published methodology in eLife, and presented a nanosymposium at SFN

## TRAININGs

**Training**: 2022 Junior Scientist Workshop on Mechanistic Cognitive Neuroscience, 2022 Cajal Neuroscience Quantitative Approaches to Behaviour